

CRF Errors Corrected by the STIC Systems Branch

JUN 18 2001

Serial Number: 09/242,454ACRF Processing Date: 5/30/2001Edited by: ARCH CENTERVerified by: 1600/2900

ENTERED

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☐Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_☐

Inserted mandatory headings, specifically: \_\_\_\_\_

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_☒Other: Seq 2,7 - deleted erroneous CDS sections

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1653

## RAW SEQUENCE LISTING

DATE: 05/30/2001

PATENT APPLICATION: US/09/742,454A

TIME: 11:45:06

Input Set : A:\2968-B Sequence Listing 4-20-01.txt

Output Set: C:\CRF3\05302001\I742454A.raw

Does Not Comply  
Corrected Diskette Needed

```

3 <110> APPLICANT: WILEY, Steven R.
5 <120> TITLE OF INVENTION: TWEAK Receptor
7 <130> FILE REFERENCE: 2968-B
9 <140> CURRENT APPLICATION NUMBER: US/09/742,454A
10 <141> CURRENT FILING DATE: 2000-12-19
12 <150> PRIOR APPLICATION NUMBER: 60/172,878
13 <151> PRIOR FILING DATE: 1999-12-20
15 <150> PRIOR APPLICATION NUMBER: 60/203,347
16 <151> PRIOR FILING DATE: 2000-05-10
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 898
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (52)..(873)
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
33 fusion protein construct
35 <400> SEQUENCE: 1
36 tctcgcagggc cacgcgttta aacgtcgagg tacctatccc gggccgccac c atg gct 57
37 Met Ala
38 1
40 aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
41 Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu Leu Cys Leu
42 5 10 15
44 ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
45 Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
46 20 25 30
48 ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
49 Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
50 35 40 45 50
52 aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
53 Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
54 55 60 65
56 agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
57 Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu
58 70 75 80
60 gag ctg gtg gca gag gag gac cag gac ccg tcg gaa ctg aat ccc cag 345
61 Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln
62 85 90 95
64 aca gaa gaa agc cag gat cct gcg cct ttc ctg aac cga cta gtt cgg 393
65 Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg
66 100 105 110
68 cct cgc aga agt gca cct aaa ggc cgg aaa aca cgg gct cga aga gcg 441

```

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DATE: 05/30/2001

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TIME: 11:45:06

Input Set : A:\2968-B Sequence Listing 4-20-01.txt

Output Set: C:\CRF3\05302001\I742454A.raw

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69 Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala
70 115          120          125          130
72 atc gca gcc cat tat gaa gtt cat cca cga cct gga cag gac gga gcg 489
73 Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala
74          135          140          145
76 cag gca ggt gtg gac ggg aca gtg agt ggc tgg gag gaa gcc aga atc 537
77 Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile
78          150          155          160
80 aac agc tcc agc cct ctg cgc tac aac cgc cag atc ggg gag ttt ata 585
81 Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile
82          165          170          175
84 gtc acc cgg gct ggg ctc tac tac ctg tac tgt cag gtg cac ttt gat 633
85 Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp
86          180          185          190
88 gag ggg aag gct gtc tac ctg aag ctg gac ttg ctg gtg gat ggt gtg 681
89 Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val
90 195          200          205          210
92 ctg gcc ctg cgc tgc ctg gag gaa ttc tca gcc act gcg gcc agt tcc 729
93 Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser
94          215          220          225
96 ctc ggg ccc cag ctc cgc ctc tgc cag gtg tct ggg ctg ttg gcc ctg 777
97 Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu
98          230          235          240
100 cgg cca ggg tcc tcc ctg cgg atc cgc acc ctc ccc tgg gcc cat ctc 825
101 Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu
102          245          250          255
104 aag gct gcc ccc ttc ctc acc tac ttc gga ctc ttc cag gtt cac tga 873
105 Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
106          260          265          270
108 gcggccgcgg atctgtttaa actag 898
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 273
113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <221> NAME/KEY: CDS
W--> 118 <222> LOCATION: (52)..(873) delete
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
122 fusion protein construct
124 <400> SEQUENCE: 2
125 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
126 1          5          10          15
128 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met
129          20          25          30
131 Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
132          35          40          45
134 Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
135          50          55          60

```

## RAW SEQUENCE LISTING

DATE: 05/30/2001

PATENT APPLICATION: US/09/742,454A

TIME: 11:45:06

Input Set : A:\2968-B Sequence Listing 4-20-01.txt

Output Set: C:\CRF3\05302001\I742454A.raw

```

137 Arg Ser Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala
138 65 70 75 80
140 Gln Glu Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn
141 85 90 95
143 Pro Gln Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu
144 100 105 110
146 Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg
147 115 120 125
149 Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
150 130 135 140
152 Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala
153 145 150 155 160
155 Arg Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu
156 165 170 175
158 Phe Ile Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
159 180 185 190
161 Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp
162 195 200 205
164 Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
165 210 215 220
167 Ser Ser Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
168 225 230 235 240
170 Ala Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
171 245 250 255
173 His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
174 260 265 270
176 His
179 <210> SEQ ID NO: 3
180 <211> LENGTH: 868
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <220> FEATURE:
185 <221> NAME/KEY: CDS
186 <222> LOCATION: (53)..(442)
188 <400> SEQUENCE: 3
189 gcttgaattc aataactata acggtcctaa ggtagcgaag aggacgtgca ct atg gct 58
190 Met Ala
191 1
193 cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106
194 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
195 5 10 15
197 ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154
198 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
199 20 25 30
201 ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
202 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
203 35 40 45 50
205 gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
206 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly

```

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TIME: 11:45:06

Input Set : A:\2968-B Sequence Listing 4-20-01.txt

Output Set: C:\CRF3\05302001\I742454A.raw

```

207          55          60          65
209 tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
210 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu
211          70          75          80
213 ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
214 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
215          85          90          95
217 ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394
218 Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile
219          100          105          110
221 gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
222 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
223 115          120          125
225 caatgtgccc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502
227 cagtctctgc ctcccagacg cggcgggagc caagctcctc caaccacaag ggggggtggg 562
229 ggcggtgaat cacctctgag gcctgggccc aggggttcagg ggaaccttcc aagggtgtctg 622
231 gttgccctgc ctctggctcc agaacagaaa gggagcctca cgctggctca cacaaaacag 682
233 ctgacactga ctaaggaact gcagcatttg cacaggggag gggggtgccc tccttcctag 742
235 aggccctggg ggccaggctg acttgggggg cagacttgac actaggcccc actcactcag 802
237 atgtcctgaa attccaccac gggggtcacc ctgggggggtt agggacctat ttttaacact 862
239 agaggg 868
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 129
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 4
248 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
249 1 5 10 15
251 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
252 20 25 30
254 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
255 35 40 45
257 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
258 50 55 60
260 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
261 65 70 75 80
263 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
264 85 90 95
266 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
267 100 105 110
269 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
270 115 120 125
272 Gln
275 <210> SEQ ID NO: 5
276 <211> LENGTH: 129
277 <212> TYPE: PRT
278 <213> ORGANISM: Mus sp.
280 <400> SEQUENCE: 5
281 Met Ala Pro Gly Trp Pro Arg Ser Leu Pro Gln Ile Leu Val Leu Gly

```

## RAW SEQUENCE LISTING

DATE: 05/30/2001

PATENT APPLICATION: US/09/742,454A

TIME: 11:45:06

Input Set : A:\2968-B Sequence Listing 4-20-01.txt

Output Set: C:\CRF3\05302001\I742454A.raw

```

282   1           5           10           15
284 Phe Gly Leu Val Leu Met Arg Ala Ala Gly Glu Gln Ala Pro Gly
285           20           25           30
287 Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
288           35           40           45
290 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys
291           50           55           60
293 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro
294   65           70           75           80
296 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser
297           85           90           95
299 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
300           100          105          110
302 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile
303           115          120          125
305 Gln
308 <210> SEQ ID NO: 6
309 <211> LENGTH: 932
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <221> NAME/KEY: CDS
315 <222> LOCATION: (1)..(930)
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
319     receptor fusion protein construct
321 <400> SEQUENCE: 6
322 atg gct cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg   48
323 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
324   1           5           10           15
326 ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc   96
327 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
328           20           25           30
330 acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag   144
331 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
332           35           40           45
334 tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc   192
335 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
336           50           55           60
338 ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga   240
339 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
340   65           70           75           80
342 tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc   288
343 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
344           85           90           95
346 gag ggc gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc   336
347 Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
348           100          105          110
350 ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg   384

```

## VERIFICATION SUMMARY

DATE: 05/30/2001

PATENT APPLICATION: US/09/742,454A

TIME: 11:45:07

Input Set : A:\2968-B Sequence Listing 4-20-01.txt

Output Set: C:\CRF3\05302001\I742454A.raw

L:118 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:2, CDS LOCATION: (52)..  
(873)

L:400 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6

L:410 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (1)..  
(930)